

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.
- (ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3
WITH INCREASED IMMUNOGENICITY AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 60 State Street, Suite 510
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/101,624;
 - (B) FILING DATE: 26-JUL-1993;
 - (A) APPLICATION NUMBER: 08/109,393;
 - (b) FILING DATE: 19-AUG-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mandragouras, Amy E.
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: RPI-008
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 227-7400
 - (B) TELEFAX: (617) 227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT      60
GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC      115
                                     Met Asp Pro
                                     1

CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG      163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
      5                      10                      15

CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT      211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
      20                      25                      30                      35

GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT      259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
                        40                      45                      50

GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG      307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
                        55                      60                      65

GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG      355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
      70                      75                      80

GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT      403
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
      85                      90                      95

CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA      451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
      100                      105                      110                      115

AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA      499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
                        120                      125                      130

GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA      547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile
                        135                      140                      145

ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC      595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr
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150					155					160						
CCA	GAA	CCT	AAG	AAG	ATG	AGT	GTT	TTG	CTA	AGA	ACC	AAG	AAT	TCA	ACT	643
Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	
165					170					175						
ATC	GAG	TAT	GAT	GGT	ATT	ATG	CAG	AAA	TCT	CAA	GAT	AAT	GTC	ACA	GAA	691
Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	
180					185					190					195	
CTG	TAC	GAC	GTT	TCC	ATC	AGC	TTG	TCT	GTT	TCA	TTC	CCT	GAT	GTT	ACG	739
Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	
					200					205					210	
AGC	AAT	ATG	ACC	ATC	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	787
Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	
215					220					225						
TTA	TCT	TCA	CCT	TTC	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	835
Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	
230					235					240						
GAC	CAC	ATT	CCT	TGG	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	883
Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	
245					250					255						
GTG	ATG	GTT	TTC	TGT	CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG	931
Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	
260					265					270					275	
CCT	CGC	AAC	TCT	TAT	AAA	TGT	GGA	ACC	AAC	ACA	ATG	GAG	AGG	GAA	GAG	979
Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	
280					285					290						
AGT	GAA	CAG	ACC	AAG	AAA	AGA	GAA	AAA	ATC	CAT	ATA	CCT	GAA	AGA	TCT	1027
Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	
295					300					305						
GAT	GAA	GCC	CAG	CGT	GTT	TTT	AAA	AGT	TCG	AAG	ACA	TCT	TCA	TGC	GAC	1075
Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	
310					315					320						
AAA	AGT	GAT	ACA	TGT	TTT	TAATTAAAGA	GTAAAGCCCA	AAAAAAA								1120
Lys	Ser	Asp	Thr	Cys	Phe											
325																

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Pro	Gln	Cys	Thr	Met	Gly	Leu	Ser	Asn	Ile	Leu	Phe	Val	Met
1				5					10					15	
Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe

20					25					30						
Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln	
		35					40					45				
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	
	50					55					60					
Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	
65					70					75					80	
Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	
				85					90					95		
Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	
			100					105					110			
His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	
		115					120					125				
Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	
	130					135					140					
Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	
145					150					155					160	
His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	
				165					170					175		
Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	
			180					185					190			
Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	
		195					200					205				
Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	
	210					215					220					
Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	
225					230					235					240	
Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	
				245					250					255		
Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	
			260					265					270			
Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	
		275					280					285				
Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	
	290					295					300					
Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	
305					310					315					320	
Ser	Cys	Asp	Lys	Ser	Asp	Thr	Cys	Phe								
				325												

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 99..1028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT	60
CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC	104
Met Asp	
1	
CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG	152
Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu	
5 10 15	
CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG	200
Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly	
20 25 30	
ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG	248
Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu	
35 40 45 50	
AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC	296
Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr	
55 60 65	
GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC	342
Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr	
70 75 80	
CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC	382
Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His	
85 90 95	
AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA	440
Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys	
100 105 110	
AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG	488
Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu	
115 120 125 130	
TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT	536
Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn	
135 140 145	
GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT	584
Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly	
150 155 160	

CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT	632
His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn	
165 170 175	
GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG	680
Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu	
180 185 190	
TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG	728
Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp	
195 200 205 210	
CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC	776
His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser	
215 220 225	
TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT	814
Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr	
230 235 240	
TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG	872
Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met	
245 250 255	
CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC	920
Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro	
260 265 270	
AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG	968
Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu	
275 280 285 290	
ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA	1016
Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro	
295 300 305	
AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT	1065
Asn Ala Glu	
TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA	1115
ATTCTACAGT TGAATAATTA AAGAAC	1151

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Pro	Arg	Cys	Thr	Met	Gly	Leu	Ala	Ile	Leu	Ile	Phe	Val	Thr		
1				5					10					15			
Val	Leu	Leu	Ile	Ser	Asp	Ala	Val	Ser	Val	Glu	Thr	Gln	Ala	Tyr	Phe		
			20					25					30				
Asn	Gly	Thr	Ala	Tyr	Leu	Pro	Cys	Pro	Phe	Thr	Lys	Ala	Gln	Asn	Ile		
		35					40					45					
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Gln	Lys	Leu	Val		
	50					55					60						
Leu	Tyr	Glu	His	Tyr	Leu	Gly	Thr	Glu	Lys	Leu	Asp	Ser	Val	Asn	Ala		
65					70				75						80		
Lys	Tyr	Leu	Gly	Arg	Thr	Ser	Phe	Asp	Arg	Asn	Asn	Trp	Thr	Leu	Arg		
				85					90					95			
Leu	His	Asn	Val	Gln	Ile	Lys	Asp	Met	Gly	Ser	Tyr	Asp	Cys	Phe	Ile		
			100					105					110				
Gln	Lys	Lys	Pro	Pro	Thr	Gly	Ser	Ile	Ile	Leu	Gln	Gln	Thr	Leu	Thr		
		115					120					125					
Glu	Leu	Ser	Val	Ile	Ala	Asn	Phe	Ser	Glu	Pro	Glu	Ile	Lys	Leu	Ala		
	130					135					140						
Gln	Asn	Val	Thr	Gly	Asn	Ser	Gly	Ile	Asn	Leu	Thr	Cys	Thr	Ser	Lys		
145					150					155					160		
Gln	Gly	His	Pro	Lys	Pro	Lys	Lys	Met	Tyr	Phe	Leu	Ile	Thr	Asn	Ser		
				165					170					175			
Thr	Asn	Glu	Tyr	Gly	Asp	Asn	Met	Gln	Ile	Ser	Gln	Asp	Asn	Val	Thr		
		180						185					190				
Glu	Leu	Phe	Ser	Ile	Ser	Asn	Ser	Leu	Ser	Leu	Ser	Phe	Pro	Asp	Gly		
		195					200					205					
Val	Trp	His	Met	Thr	Val	Val	Cys	Val	Leu	Glu	Thr	Glu	Ser	Met	Lys		
	210					215					220						
Ile	Ser	Ser	Lys	Pro	Leu	Asn	Phe	Thr	Gln	Glu	Phe	Pro	Ser	Pro	Gln		
225					230					235					240		
Thr	Tyr	Trp	Lys	Glu	Ile	Thr	Ala	Ser	Val	Thr	Val	Ala	Leu	Leu	Leu		
				245					250					255			
Val	Met	Leu	Leu	Ile	Ile	Val	Cys	His	Lys	Lys	Pro	Asn	Gln	Pro	Ser		
			260					265					270				

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
 275 280 285

Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
 290 295 300

Lys Pro Asn Ala Glu
 305

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAAAGAAAA AGTGATTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60

GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120

GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180

GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240

TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGGCTTT CACTTTTGAC 300

CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
 -30 -25

AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401
 Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
 -20 -15 -10

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449
 Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
 -5 1 5 10

GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 497
 Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala

	15	20	25	
CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG				545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met	30	35	40	
ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC				593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile	45	50	55	
TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA				641
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro	60	65	70	
TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC				689
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp	75	80	85	90
GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT				737
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala	95	100	105	
GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT				785
Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn	110	115	120	
ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC				833
Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His	125	130	135	
CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA				881
Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr	140	145	150	
GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG				929
Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu	155	160	165	170
GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT				977
Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr	175	180	185	
GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA				1025
Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln	190	195	200	
GAG CAT TTT CCT GAT AAC CTG CTC CCA TCC TGG GCC ATT ACC TTA ATC				1073

Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile
 205 210 215

TCA GTA AAT GGA ATT TTT GTG ATA TGC TGC CTG ACC TAC TGC TTT GCC 1121
 Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala
 220 225 230

CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA AGT 1169
 Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser
 235 240 245 250

GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA 1221
 Val Arg Pro Val

GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC 1281

CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT CTTTCAGATT 1341

AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT 1401

TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461

AATTCATTAT CTATTAAACA CTAATTTGAG 1491

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 -30 -25 -20

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 -15 -10 -5

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 -1 1 5 10

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 15 20 25 30

Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr	Met	Met	Ser	Gly	Asp		
				35					40					45			
Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Ile	Phe	Asp	Ile	Thr		
			50					55					60				
Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly		
		65					70					75					
Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg		
	80					85					90						
Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr		
	95				100					105					110		
Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile		
				115					120					125			
Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu		
			130					135					140				
Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp		
		145					150					155					
Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met		
	160					165					170						
Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	Gly	His	Leu	Arg		
	175				180					185					190		
Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	Glu	His	Phe	Pro		
				195					200					205			
Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile	Ser	Val	Asn	Gly		
		210						215					220				
Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala	Pro	Arg	Cys	Arg		
	225						230					235					
Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser	Val	Arg	Pro	Val		
	240					245					250						

(8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus
 (D) DEVELOPMENTAL STAGE: germ line
 (F) TISSUE TYPE: lymphoid
 (G) CELL TYPE: B lymphocyte
 (H) CELL LINE: 70Z and A20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC	60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG	120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA	180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT	240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC	290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu	
-35 -30 -25	
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT	338
Lys Phe Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg	
-20 -15 -10	
CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG	386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	
-5 -1 1 5	
AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT	434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp	
10 15 20 25	
GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG	482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu	
30 35 40	
TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG	530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg	
45 50 55	
ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC	578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val	
60 65 70	
CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA	626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	
75 80 85	
GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA	674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	
90 95 100 105	

GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA	722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	
110 115 120	
GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT	770
Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro	
125 130 135	
CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG	818
Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	
140 145 150	
ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA	866
Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	
155 160 165	
CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA	914
Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	
170 175 180 185	
TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA	962
Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	
190 195 200	
GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA	1010
Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly	
205 210 215	
TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC	1058
Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys	
220 225 230	
TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA	1106
Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu	
235 240 245	
ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG	1154
Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln	
250 255 260 265	
ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG	1206
Thr Val Phe Leu	
GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	1266
ACAAGATAGA GTTAAGTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1326
CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	1386
ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA	1446
GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGTTG	1506
GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG	1566
GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG	1626
GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG	1686

(9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 -35 -30 -25

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 -20 -15 -10

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 -5 -1 1 5 10

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 15 20 25

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 30 35 40

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 45 50 55

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 60 65 70 75

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
 80 85 90

Tyr Gly Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
 95 100 105

Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
 110 115 120

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
 125 130 135

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
 140 145 150 155

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
 160 165 170

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
 175 180 185

Asp	Ala	His	Val	Ser	Glu	Asp	Phe	Thr	Trp	Glu	Lys	Pro	Pro	Glu	Asp
		190					195					200			
Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu	Phe	Gly	Ala	Gly	Phe	Gly
	205					210					215				
Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val	Ile	Ile	Lys	Cys	Phe	Cys
220					225					230					235
Lys	His	Arg	Ser	Cys	Phe	Arg	Arg	Asn	Glu	Ala	Ser	Arg	Glu	Thr	Asn
				240					245					250	
Asn	Ser	Leu	Thr	Phe	Gly	Pro	Glu	Glu	Ala	Leu	Ala	Glu	Gln	Thr	Val
			255					260					265		
Phe	Leu														